RAW SEQUENCE LISTING ERROR REPORT
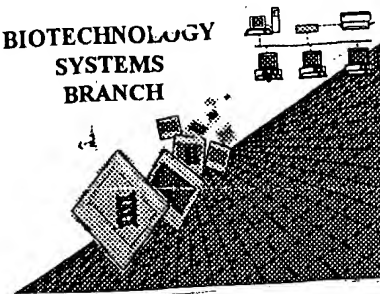
BIOTECHNOLOGY SYSTEMS BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/977,137_

Source: _OIPE_

Date Processed by STIC: _11/1/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS. PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: **patin21help@uspto.gov** or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: **patin3help@uspto.gov** or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

OIPE

RAW SEQUENCE LISTING   DATE: 11/01/2001
PATENT APPLICATION: US/09/977,137   TIME: 08:32:44

Input Set : A:\ES.txt
Output Set: N:\CRF3\11012001\I977137.raw   *Does Not Comply*
Corrected Diskette Needed

```
 3 <110> APPLICANT: Summers, Anne O.
 4        Caguiat, Jonathan
 6 <120> TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
 7        Methods
 9 <130> FILE REFERENCE: 79-00
```
OK> 11 **<140> CURRENT APPLICATION NUMBER: US/09/977,137**
```
12 <141> CURRENT FILING DATE: 2001-10-12
14 <150> PRIOR APPLICATION NUMBER: US 60/240,465
15 <151> PRIOR FILING DATE: 2000-10-12
17 <160> NUMBER OF SEQ ID NOS: (18)  14 (see pp 3-5)
19 <170> SOFTWARE: PatentIn Ver. 2.0
```

ERRORED SEQUENCES

```
 89 <210> SEQ ID NO: 4
 90 <211> LENGTH: 117
 91 <212> TYPE: PRT
 92 <213> ORGANISM: Artificial Sequence
 94 <220> FEATURE:
 95 <223> OTHER INFORMATION: Description of Artificial Sequence: chelon
 97 <400> SEQUENCE: 4
 98 Met Thr His Cys Glu Glu Ala Ser Ser Leu Ala Glu His Lys Leu Lys
 99  1               5                  10              15
101 Asp Val Arg Glu Lys Met Ala Asp Leu Ala Arg Met Glu Thr Val Leu
102             20                  25              30
104 Ser Glu Leu Val Cys Ala Cys His Ala Arg Lys Gly Asn Val Ser Cys
105         35                  40                  45
107 Pro Leu Ile Ala Ser Leu Gln Gly Ser Ser Gly Thr His Cys Glu Glu
108     50                  55                  60
110 Ala Ser Ser Leu Ala Glu His Lys Leu Lys Asp Val Arg Glu Lys Met
111  65                  70                  75              80
113 Ala Asp Leu Ala Arg Met Glu Thr Val Leu Ser Glu Leu Val Cys Ala
114             85                  90                  95
116 Cys His Ala Arg Lys Gly Asn Val Ser Cys Pro Ser Ala Trp Ser His
117             100                 105             110
```
E--> 119 Pro Gln Phe Glu Lys   *115 (insert)*

What is this? delete

SEQUENCE LISTING

W--> 121 <110> ~~APPLICANT: Summers, Anne O.~~
W--> 121 **<110> APPLICANT: Summers, Anne O.**
W--> 124 <120> ~~TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and~~
W--> 124 **<120> TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and**
W--> 125   **Methods**
W--> 127 <130> ~~FILE REFERENCE: 79-00~~
W--> 127 **<130> FILE REFERENCE: 79-00**
W--> 129 **<140> CURRENT APPLICATION NUMBER: unassigned**
     130 <141> CURRENT FILING DATE: 2001-10-12
W--> 132 **<150> PRIOR APPLICATION NUMBER: US 60/240,465**

see next page

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/977,137

DATE: 11/01/2001
TIME: 08:32:44

Input Set : A:\ES.txt
Output Set: N:\CRF3\11012001\I977137.raw

delete

W--> 133 <151> PRIOR FILING DATE: 2000-10-12
W--> 135 <160> NUMBER OF SEQ ID NOS: 18
W--> 135 <160> NUMBER OF SEQ ID NOS: 18
W--> 137 <170> SOFTWARE: PatentIn Ver. 2.0

ignore - see pp 3-5

207 <210> SEQ ID NO: 4
208 <211> LENGTH: 117
209 <212> TYPE: PRT
210 <213> ORGANISM: Artificial Sequence
212 <220> FEATURE:
213 <223> OTHER INFORMATION: Description of Artificial Sequence: chelon
215 <400> SEQUENCE: 4
216 Met Thr His Cys Glu Glu Ala Ser Ser Leu Ala Glu His Lys Leu Lys
217 1   5   10   15
219 Asp Val Arg Glu Lys Met Ala Asp Leu Ala Arg Met Glu Thr Val Leu
220   20   25   30
222 Ser Glu Leu Val Cys Ala Cys His Ala Arg Lys Gly Asn Val Ser Cys
223   35   40   45
225 Pro Leu Ile Ala Ser Leu Gln Gly Ser Ser Gly Thr His Cys Glu Glu
226   50   55   60
228 Ala Ser Ser Leu Ala Glu His Lys Leu Lys Asp Val Arg Glu Lys Met
229 65   70   75   80
231 Ala Asp Leu Ala Arg Met Glu Thr Val Leu Ser Glu Leu Val Cys Ala
232   85   90   95
234 Cys His Ala Arg Lys Gly Asn Val Ser Cys Pro Ser Ala Trp Ser His
235   100   105   110
237 Pro Gln Phe Glu Lys
E--> 238   50   55   60
240 Ala Ser Ser Leu Ala Glu His Lys Leu Lys Asp Val Arg Glu Gln Met
E--> 241 65   70   75   80
243 Ala Asp Leu Ala Arg Met Glu Thr Val Leu Ser Glu Leu Val Cys Ala
E--> 244   85   90   95
246 Cys His Ala Arg Lys Gly Asn Val Ser Cys Pro Ser Ala Trp Ser His
E--> 247   100   105   110
249 Pro Gln Phe Glu Lys
E--> 250   115
E--> 253 <210> SEQ ID NO: 9

<170> PatentIn Ver. 2.0

<210> 1
<211> 435
<212> DNA
<213> Shigella flexneri, Tn21 of Plasmid R100

<400> 1
atggaaaata atttggaaaa cctgaccatt ggcgtttttg ccaaggcggc cggggtcaac 60
gtggagacaa tccgcttcta tcagcgcaag ggcctgttgc gggaaccgga caagccttac 120
ggcagcatcc gccgctatgg ggaggcggac gtggttcggg tgaaattcgt gaaatcggca 180
cagcggctgg ggttcagtct ggacgagatt gccgagctgt tgcggctcga cgatggcacc 240
cagcggctgg ggttcagtct ggacgagatt gccgagctgt tgcggctcga cgatggcacc 240
cactgcgagg aggccagcag cctggccgaa cacaagctca aggacgtgcg cgagaagatg 300
gccgacttgg cgcgcatgga aaccgtgctg tctgaactcg tgtgcgcctg ccatgcacga 360
aaggggaatg tttcctgccc gttgatcgcg tcactacagg gcgaagcagg cctggcaagg 420
tcagctatgc cttag 435

<210> 2
<211> 144
<212> PRT
<213> Shigella flexneri, Tn21 of Plasmid R100

<400> 2
Met Glu Asn Asn Leu Glu Asn Leu Thr Ile Gly Val Phe Ala Lys Ala
1   5   10   15

Ala Gly Val Asn Val Glu Thr Ile Arg Phe Tyr Gln Arg Lys Gly Leu
            20   25   30

Leu Arg Glu Pro Asp Lys Pro Tyr Gly Ser Ile Arg Arg Tyr Gly Glu
        35   40   45

Ala Asp Val Val Arg Val Lys Phe Val Lys Ser Ala Gln Arg Leu Gly
    50   55   60

Phe Ser Leu Asp Glu Ile Ala Glu Leu Leu Arg Leu Asp Asp Gly Thr
65   70   75   80

His Cys Glu Glu Ala Ser Ser Leu Ala Glu His Lys Leu Lys Asp Val
                85   90   95

Arg Glu Lys Met Ala Asp Leu Ala Arg Met Glu Thr Val Leu Ser Glu
            100   105   110

Leu Val Cys Ala Cys His Ala Arg Lys Gly Asn Val Ser Cys Pro Leu
            115   120   125

Ile Ala Ser Leu Gln Gly Glu Ala Gly Leu Ala Arg Ser Ala Met Pro
        130   135   140

<210> 3
<211> 321
<212> DNA

<212> Artificial Sequence

<220>
<223> Description of Artificial Sequence: chelon

<400> 3
atgacacact gcgaggaggc cagcagcctg gccgaacaca agctcaagga cgtgcgcgag 60
aagatggccg acttggcgcg catggaaacc gtgctgtctg aactcgtgtg cgcctgccat 120
gcacgaaagg ggaatgtttc ctgcccgttg atcgcgtcac tacagggatc ctcaggcacc 180
cactgcgagg aggccagcag cctggccgaa cacaagctca aggacgtgcg cgagaagatg 240
gccgacttgg cgcgcatgga aaccgtgctg tctgaactcg tgtgcgcctg ccatgcacga 300
aaggggaatg tttcctgccc g 321

<210> 4
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: chelon

<400> 4
Met Thr His Cys Glu Glu Ala Ser Ser Leu Ala Glu His Lys Leu Lys
1   5   10   15

Asp Val Arg Glu Lys Met Ala Asp Leu Ala Arg Met Glu Thr Val Leu
            20   25   30

Ser Glu Leu Val Cys Ala Cys His Ala Arg Lys Gly Asn Val Ser Cys
        35   40   45

Pro Leu Ile Ala Ser Leu Gln Gly Ser Ser Gly Thr His Cys Glu Glu
    50   55   60

Ala Ser Ser Leu Ala Glu His Lys Leu Lys Asp Val Arg Glu Lys Met
65   70   75   80

Ala Asp Leu Ala Arg Met Glu Thr Val Leu Ser Glu Leu Val Cys Ala
            85   90   95

Cys His Ala Arg Lys Gly Asn Val Ser Cys Pro Ser Ala Trp Ser His
            100   105   110

Pro Gln Phe Glu Lys   Leu Gln Gly Ser Ser Gly Thr His Cys Glu Glu
    50   55   60

Ala Ser Ser Leu Ala Glu His Lys Leu Lys Asp Val Arg Glu Gln Met
65   70   75   80

Ala Asp Leu Ala Arg Met Glu Thr Val Leu Ser Glu Leu Val Cys Ala
            85   90   95

Cys His Ala Arg Lys Gly Asn Val Ser Cys Pro Ser Ala Trp Ser His
            100   105   110

Pro Gln Phe Glu Lys
            115

: then, jumps to Sequence 9
(Sequences 5 through 8
missing)

<210> 9

Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

Input Set : **A:\ES.txt**
Output Set: **N:\CRF3\11012001\I977137.raw**

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:119 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:119 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:119 M:252 E: No. of Seq. differs, <211>LENGTH:Input:117 Found:119 SEQ:4
L:121 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:121 M:281 W: Numeric Fields not Ordered, <110> not ordered!.
L:124 M:280 W: Numeric Identifier already exists, <120> found multiple times
L:124 M:281 W: Numeric Fields not Ordered, <120> not ordered!.
L:127 M:280 W: Numeric Identifier already exists, <130> found multiple times
L:127 M:281 W: Numeric Fields not Ordered, <130> not ordered!.
L:129 M:280 W: Numeric Identifier already exists, <140> found multiple times
L:129 M:281 W: Numeric Fields not Ordered, <140> not ordered!.
L:129 M:270 C: Current Application Number differs, Replaced Current Application Number
L:130 M:280 W: Numeric Identifier already exists, <141> found multiple times
L:130 M:281 W: Numeric Fields not Ordered, <141> not ordered!.
L:132 M:281 W: Numeric Fields not Ordered, <150> not ordered!.
L:133 M:281 W: Numeric Fields not Ordered, <151> not ordered!.
L:135 M:280 W: Numeric Identifier already exists, <160> found multiple times
L:135 M:281 W: Numeric Fields not Ordered, <160> not ordered!.
L:137 M:280 W: Numeric Identifier already exists, <170> found multiple times
L:238 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
M:332 Repeated in SeqNo=4
L:250 M:252 E: No. of Seq. differs, <211>LENGTH:Input:117 Found:181 SEQ:4
L:253 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 5 thru 8

11/1/01